Amendments to the Specification:

Please replace paragraph [0072.1] with the following amended paragraph:

[0072.1] For example, ~~SNIDE~~ <u>the present invention</u> provides a method for predicting one or more locations of single nucleotide polymorphisms in a nucleic acid sequence by calculating a variation frequency from a first base to a second base within a group of bases in a dataset of two or more genes, generating a variation predictiveness matrix from the calculated variation frequency, comparing the nucleic acid sequence one or more groups at a time with the variation predictiveness matrix to assign a variation value to the bases in the nucleic acid sequence, identifying the locations of the bases in the nucleic acid sequence where single nucleotide polymorphisms will likely occur based on the assigned variation value, and outputting the identified locations of the single nucleotide polymorphisms. Note that this method can be implemented as a computer program embodied on a computer readable medium in which each step is performed by one or more code segments.